

#6



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Baker et al.) Group Art Unit Unknown
Appl. No. : 10/015,389)
Filed : December 11, 2001)
For : SECRETED AND)
TRANSMEMBRANE)
POLYPEPTIDES AND NUCLEIC)
ACIDS ENCODING THE SAME)
Examiner : Unknown)

SEQUENCE SUBMISSION STATEMENT

United States Patent and Trademark Office
PO Box 2327
Arlington, VA 22202

Dear Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, mailed March 21, 2002. I hereby state that the amendments, made in accordance with 37 C.F.R. § 1.825(a) and included in the Substitute Sequence Listing submitted herewith, are supported in the application, and that the Substitute Sequence Listing does not include new matter.

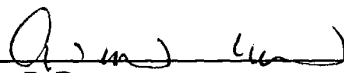
I further state that the information recorded in the currently submitted substitute copy of the computer-readable form of the Sequence Listing is identical to the paper form of the Sequence Listing submitted herewith as required in 37 C.F.R. § 1.825(b).

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: June 21, 2002

By: 
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Newport Beach, CA 92660
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Sequence Listing



<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan I.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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tatgcagtgg aaggtttcaa tgacagctta agacgggaca tgaaagcttt 700
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tctccagaca tcaaacaaca atatggagaa ggttacattg aaaaaagtct 850
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tggtagagt catggaccac gctctaaca gtctcttccc taagactcat 950
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gccagcagct ttgcaagact ttttattggt gaaacagaaa gcagagctgg 1050
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aaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171,198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
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Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe	Gly Leu Ile Ser Val	Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys	Ala Gln Gly Arg Val	Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu	Ala Ile Val Gly Gly	Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu	Gly Phe Asn Asp Ser	Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val					

<210> 11

<211> 2720

<212> DNA

<213> Homo sapiens

<400> 11

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gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150

gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
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gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
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gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
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cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala	20	25	30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro	35	40	45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr	50	55	60
Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp	65	70	75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu	80	85	90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala	95	100	105
Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile			

290										295					300				
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser					
				305					310					315					
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu					
				320					325					330					
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu					
				335					340					345					
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn					
				350					355					360					
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser					
				365					370					375					
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr					
				380					385					390					
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe					
				395					400					405					
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala					
				410					415					420					
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys					
				425					430					435					
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe					
				440					445					450					
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr					
				455					460					465					
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu					
				470					475					480					
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg					
				485					490					495					
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val					
				500					505					510					
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu					
				515					520					525					
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly					
				530					535					540					
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr					
				545					550					555					
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu					
				560					565					570					
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val					

	575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro	Glu Thr
	590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys
	605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe
	620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln
	635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe
	650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp
	665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala
	680	685	690
His Pro Leu Pro	Ile Trp Thr Pro Ala		
	695		

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 13
 cgccagaagg gcgtgattga cgtc 24

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 14
 ccaccccttct tcccagacag gccg 24

<210> 15
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtect tcagtgagtg gtttgcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250
cgggcagtca ggggacaagg gcaggagacc tcggggccctc cccgtgcctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
cccaccgcct ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400
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gcaccacatc tacgtgtca accagggtgga ccacttcagg ttcaaccggg 500
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cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
ttttccgcc ctcgggaatc acaactgggt acaagacatt tcgccacctg 850
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cgctgcttgc catgcacagt gatcagagag aggctgggggt gtgtcctgtc 1300
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 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17

<211> 327

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-42

<223> Signal peptide.

<220>

<221> misc_feature

<222> 19-25,65-71,247-253,285-291,303-310

<223> N-myristoylation site.

<220>

<221> misc_feature

<222> 27-31

<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>

<221> TRANSMEM

<222> 29-49

<223> Transmembrane domain (type II).

<220>

<221> misc_feature

<222> 154-158

<223> N-glycosylation site.

<220>

<221> misc_feature

<222> 226-233

<223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp
1				5					10				15	

Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser
			20						25				30	

Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser
			35						40				45	

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala			50	55	60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys			65	70	75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp			80	85	90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe			95	100	105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser			110	115	120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp			125	130	135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu			140	145	150
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp			155	160	165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala			170	175	180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His			185	190	195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His			200	205	210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly			215	220	225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu			230	235	240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe			245	250	255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg			260	265	270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly			275	280	285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu			290	295	300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp			305	310	315
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser						320	325	

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
gcgaacgctt cgaggagtcc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg cactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag ccagccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagatagga acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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<211> 616

<212> PRT

<213> Homo sapiens

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<222> 1-33

<223> Signal peptide.

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<221> TRANSMEM

<222> 13-40

<223> Transmembrane domain (type II).

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Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn
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Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser
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Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp
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Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp
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Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val	
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Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr	
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Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu	
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Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala	
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg	
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Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met	
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly	
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575 580 585

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<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<221> sig_peptide

<222> 1-21

<223> Signal peptide.

<400> 29

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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
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Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
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Lys Gly Ser Gln Lys Ser
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<212> DNA

<213> Homo sapiens

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<211> 322
<212> PRT
<213> Homo sapiens

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Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
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Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105

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Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp	125	130	135
His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala	140	145	150
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile	155	160	165
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu	170	175	180
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn	185	190	195
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr	200	205	210
Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu	215	220	225
Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu	230	235	240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu	245	250	255
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln	260	265	270
Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr	275	280	285
Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr	290	295	300
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<211> 3680

<212> DNA

<213> Homo sapiens

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<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
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His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
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Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
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Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
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Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg	125	130	135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys	140	145	150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp	155	160	165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala	170	175	180
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His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu	200	205	210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser	215	220	225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu	230	235	240
Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro	245	250	255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala	260	265	270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser	275	280	285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu	290	295	300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser	305	310	315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala	320	325	330
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 34

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<210> 37
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<400> 37
ggcgagccct aactatccag gag 23

<210> 38
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<212> DNA
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<400> 39
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<210> 40
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<212> DNA

<213> Homo sapiens

<400> 40

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<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

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35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105

Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val	
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Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser	
				125					130					135	
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr	
				140					145					150	
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser	
				155					160					165	
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val	
				170					175					180	
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser	
				185					190					195	
Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu	
				200					205					210	
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn	
				215					220					225	
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe	
				230					235					240	
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu	
				245					250					255	
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser	
				260					265					270	
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu	
				275					280					285	
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser	
				290					295					300	
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu	
				305					310					315	
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 <212> DNA
 <213> Homo sapiens

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<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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				20					25					30
Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45
Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
				50					55					60
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
				65					70					75
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
				80					85					90
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
				95					100					105
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
				110					115					120
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
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Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
				140					145					150
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
				155					160					165
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
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Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
				185					190					195
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
				200					205					210
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
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Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 44

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<210> 45
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 45

gggaactgct atctgatgcc 20

<210> 46
 <211> 26
 <212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 46

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<210> 47
 <211> 28
 <212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 47

cttctcgaac cacataagtt tgaggcag 28

<210> 48
 <211> 25
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

cacgattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

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				20				25					30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu
				35				40					45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro
				50				55					60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly
				65				70					75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe

	80	85	90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala	95	100	105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln	110	115	120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys	125	130	135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe	140	145	150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala	155	160	165
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr	170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp	185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys	200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro	215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu	230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly	245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro	260	265	270
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<212> DNA

<213> Homo sapiens

<400> 51

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<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

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Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
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Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
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Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
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Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
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Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
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Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
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 <212> DNA
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<211> 280

<212> PRT

<213> Homo sapiens

<400> 54

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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
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				80					85				90	
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100				105	
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115				120	
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130				135	
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145				150	

Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu	155	160	165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu	170	175	180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala	185	190	195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg	200	205	210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala	215	220	225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp	230	235	240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala	245	250	255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala	260	265	270
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<212> DNA

<213> Homo sapiens

<400> 55

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<211> 299

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<213> Homo sapiens

<400> 56

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Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg	35	40	45	
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro	50	55	60	
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val	65	70	75	
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro	80	85	90	
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	95	100	105	
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg	110	115	120	
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln	125	130	135	
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Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val	155	160	165	
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala				

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	200		205		210
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Arg Leu Gln Arg	Met Pro Tyr His Tyr	Tyr Glu Pro Lys Gly Pro			
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Asp Glu Cys Val	Thr Tyr Ile Gln Asn	Glu His Ser Arg Lys Gly			
	260		265		270
Asn His His Arg	Phe Ile Thr Glu Lys	Arg Val Phe Ser Ser Trp			
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<210> 58

<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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				20					25					30
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
				35					40					45
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
				50					55					60
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
				65					70					75
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
				80					85					90

Leu Val Ile Thr	Ala	Leu Asn Asn His	Thr Val Gly Arg Tyr Gln
	95		100 105
Cys Val Ala Arg	Met	Pro Ala Gly Ala	Val Ala Ser Val Pro Ala
	110		115 120
Thr Val Thr Leu	Ala Asn Leu Gln Asp	Phe Lys Leu Asp	Val Gln
	125	130	135
His Val Ile Glu	Val Asp Glu Gly Asn	Thr Ala Val Ile Ala	Cys
	140	145	150
His Leu Pro Glu	Ser His Pro Lys Ala	Gln Val Arg Tyr Ser	Val
	155	160	165
Lys Gln Glu Trp	Leu Glu Ala Ser Arg	Gly Asn Tyr Leu Ile	Met
	170	175	180
Pro Ser Gly Asn	Leu Gln Ile Val Asn	Ala Ser Gln Glu Asp	Glu
	185	190	195
Gly Met Tyr Lys	Cys Ala Ala Tyr Asn	Pro Val Thr Gln Glu	Val
	200	205	210
Lys Thr Ser Gly	Ser Ser Asp Arg Leu	Arg Val Arg Arg Ser	Thr
	215	220	225
Ala Glu Ala Ala	Arg Ile Ile Tyr Pro	Pro Glu Ala Gln Thr	Ile
	230	235	240
Ile Val Thr Lys	Gly Gln Ser Leu Ile	Leu Glu Cys Val Ala	Ser
	245	250	255
Gly Ile Pro Pro	Pro Arg Val Thr Trp	Ala Lys Asp Gly Ser	Ser
	260	265	270
Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr
	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
	365	370	375

Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	
				380					385					390	
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	
				395					400					405	
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	
				410					415					420	
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	
				425					430					435	
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	
				440					445					450	
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	
				455					460					465	
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	
				470					475					480	
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	
				485					490					495	
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	
				500					505					510	
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	
				515					520					525	
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	
				530					535					540	
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	
				545					550					555	
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg	
				560					565					570	
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln	
				575					580					585	
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp	
				590					595					600	
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile	
				605					610					615	
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg	
				620					625					630	
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys	
				635					640					645	
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile	
				650					655					660	

Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly
 665 670 675
 Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu
 680 685 690
 Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr
 695 700 705
 Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr
 710 715 720
 Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met
 725 730 735
 Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr
 740 745 750
 Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys
 755 760 765
 Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
 770 775 780
 Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn
 785 790 795
 Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr
 800 805 810
 Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro
 815 820 825
 Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg
 830 835 840
 Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro
 845 850 855
 Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu	950	955	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His	965	970	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly	980	985	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro	995	1000	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys	1010	1015	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg	1025	1030	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro	1040	1045	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu	1055	1060	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp	1070	1075	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly	1085	1090	1095
Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr	1100	1105	1110
Pro Pro Leu Thr Ile	1115		

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
caccccaaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
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cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100
cacggggcgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgtc 150
tgctgtctct gctactgctg ctgctgctgc ggcagcccgt aaccgcgcgc 200
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccacg 250
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ctacgccagg cacccccaaa accctggacc ttccggggtcg cgcgcaggcc 350
ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgcccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
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 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63

<211> 487

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 196, 386

<223> unknown amino acid

<400> 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg
				20					25					30

Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
				35					40					45

Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
				50					55					60

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro			
				65					70					75			
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser			
				80					85					90			
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg			
				95					100					105			
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe			
				110					115					120			
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val			
				125					130					135			
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp			
				140					145					150			
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His			
				155					160					165			
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala			
				170					175					180			
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val			
				185					190					195			
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser			
				200					205					210			
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys			
				215					220					225			
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met			
				230					235					240			
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val			
				245					250					255			
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala			
				260					265					270			
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro			
				275					280					285			
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu			
				290					295					300			
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly			
				305					310					315			
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu			
				320					325					330			
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg			
				335					340					345			

Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp
350		355 360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	
365		370 375
Pro Val Leu Ile	Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu	
380		385 390
Glu Leu Gln Gly	Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	
395		400 405
Gln Val Glu Lys	Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val	
410		415 420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser	
425		430 435
His Leu Val Pro	Gln Asn Gly His Gln Ala Thr His Leu Glu Val	
440		445 450
Thr Lys Gln Pro	Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala	
455		460 465
Ser Pro Tyr Leu Val	Pro Gly Leu Val Ala Ala Ala Thr Ile Pro	
470		475 480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 64
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<210> 65
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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 <211> 183
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 80 85 90
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 95 100 105
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 110 115 120
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 125 130 135
 Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
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Met Leu Ser

<210> 69

<211> 3170

<212> DNA

<213> Homo sapiens

<400> 69

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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly
				50					55					60

Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala
				65					70					75

Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys
				80					85					90

His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg
				95					100					105

Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr
				110					115					120

Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
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Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145					150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160					165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175					180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190					195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205					210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220					225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235					240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
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Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
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Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
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Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
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Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
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Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
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Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
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Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
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Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
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Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
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Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
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Ser Pro Val Ser	Ser Ser Glu Ser Ala	Pro Gly Thr Ile Met	Asn		
	305		310		315
Gly His Gly Gly	Gly Arg Ser Gln Gln	Thr Leu Asp Ser Lys	Tyr		
	320		325		330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu	Val Pro Thr Lys Gln	Arg		
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Lys Arg Ile Ala	His Val Met Trp Lys	Thr Pro Val Gly Gln	Trp		
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Leu Ile Arg

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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 73
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<210> 74
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 74
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<210> 75
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 <212> DNA
 <213> Artificial Sequence

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<210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

<400> 76

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<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu	35	40	45	
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro	50	55	60	
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val	65	70	75	
Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His	80	85	90	
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His	95	100	105	
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg	110	115	120	
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro	125	130	135	

Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu	140	145	150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp	155	160	165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu	170	175	180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala	185	190	195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser	200	205	210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val	215	220	225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln	230	235	240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu	245	250	255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu	260	265	270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn	275	280	285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg	290	295	300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu	305	310	315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp	320	325	330
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<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

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				20					25					30
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
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Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
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Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
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Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
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Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
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Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val
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Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val
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Val	Arg	Asn	Ser	Ala 230	Leu	Ala	Phe	Phe	Leu 235	Thr	Ala	Thr	Ile	Phe 240
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Ile	Leu	Lys	Lys	Thr 305	Ala	Ser	Leu	Gly	Phe 310	Cys	Val	Thr	Tyr	Val 315
Phe	Phe	Ile	Thr	Ser 320	Leu	Ile	Tyr	Pro	Ala 325	Val	Cys	Thr	Asn	Ile 330
Glu	Ser	Leu	Asn	Lys 335	Gly	Ser	Gly	Ser	Leu 340	Trp	Thr	Thr	Lys	Phe 345
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Ser	Lys	Ala	Leu	Pro 380	Gly	Phe	Val	Leu	Leu 385	Arg	Thr	Cys	Leu	Ile 390
Pro	Leu	Phe	Val	Leu 395	Cys	Asn	Tyr	Gln	Pro 400	Arg	Val	His	Leu	Lys 405
Thr	Val	Val	Phe	Gln 410	Ser	Asp	Val	Tyr	Pro 415	Ala	Leu	Leu	Ser	Ser 420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
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Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
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455 460 465

Ala Cys Ser Thr Leu Leu Val His Leu Ile
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<212> DNA

<213> Homo sapiens

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 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
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 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
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 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
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 185 190 195

Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr	200	205	210
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala	215	220	225
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr	230	235	240
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp	245	250	255
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro	260	265	270
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala	275	280	285
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln	290	295	300
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Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
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<211> 3316

<212> DNA

<213> Homo sapiens

<400> 85

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<210> 86
 <211> 739
 <212> PRT
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<400> 86
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 Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser

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Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile					
				50					55					60					
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys					
				65					70					75					
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg					
				80					85					90					
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val					
				95					100					105					
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn					
				110					115					120					
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu					
				125					130					135					
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu					
				140					145					150					
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys					
				155					160					165					
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His					
				170					175					180					
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala					
				185					190					195					
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr					
				200					205					210					
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu					
				215					220					225					
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile					
				230					235					240					
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu					
				245					250					255					
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro					
				260					265					270					
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu					
				275					280					285					
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe					
				290					295					300					
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys					
				305					310					315					
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr					

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His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val	335		340		345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr	350		355		360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val	365		370		375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg	380		385		390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro	395		400		405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn	410		415		420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val	425		430		435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp	440		445		450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu	455		460		465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser	470		475		480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val	485		490		495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe	500		505		510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu	515		520		525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr	530		535		540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn	545		550		555
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala	560		565		570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp	575		580		585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile	590		595		600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu					

605										610					615				
Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His					
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				635					640					645					
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly					
				650					655					660					
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile					
				665					670					675					
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr					
				680					685					690					
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser					
				695					700					705					
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly					
				710					715					720					
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu					
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His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

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 ccaggacatt ggtgaccgc caatccggta tggacgactg gaagcccagc 150
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 cagggggcgt gcttttctctg ctggtgactg tcattgtcaa tatcaagttg 300
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105

Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu	110	115	120
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val	125	130	135
Leu	Asn	Gln	Ala	Thr	Gly	His	Val	Met	Ala	Lys	Arg	Val	Phe	Asp	140	145	150
Thr	Tyr	Ser	Pro	His	Glu	Asp	Glu	Ala	Met	Val	Leu	Phe	Leu	Asn	155	160	165
Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Cys	Thr	Val	Lys	Asp	Glu	170	175	180
Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser	185	190	195
Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Arg	Asp	Thr	Trp	200	205	210
Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu	Lys	His	215	220	225
Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val	Leu	Leu	230	235	240
Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His	245	250	255
Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Phe	Cys	Ser	260	265	270
Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp	Pro	Thr	275	280	285
Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys	Val	Leu	290	295	300
Asn	Val	Pro	Val	Ala	Val	Ile	Ala	Gly	Asn	Arg	Pro	Asn	Tyr	Leu	305	310	315
Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro	320	325	330
Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu	Pro	Met	335	340	345
Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His	Thr	Pro	350	355	360
Ile	Ser	Ile	Lys	Asn	Ala	Arg	Val	Ser	Gln	His	Tyr	Lys	Ala	Ser	365	370	375
Leu	Thr	Ala	Thr	Phe	Asn	Leu	Phe	Pro	Glu	Ala	Lys	Phe	Ala	Val	380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe		395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr		410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu		425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly		440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys		455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg		470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val		485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly		500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val		515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala		530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu		545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr		560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp		575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp		590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe		605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro		620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu		635	640	645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr		650	655	660

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<211> 25

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

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<210> 91
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<212> DNA
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<223> Synthetic oligonucleotide probe

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<210> 92
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<212> DNA
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<210> 93
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<212> DNA
<213> Artificial Sequence

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<210> 94
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<212> DNA
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<400> 94

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<210> 95

<211> 307

<212> PRT

<213> Homo sapiens

<400> 95

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Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe	20	25	30	
Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	35	40	45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	50	55	60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	65	70	75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	80	85	90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	95	100	105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu	110	115	120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	125	130	135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	155	160	165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	170	175	180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	185	190	195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	

Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
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Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val
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Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu
245 250 255

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260 265 270

His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg
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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
				50					55					60
Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
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Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
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Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
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Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
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Glu Val Val Leu	Asp Ser Lys Arg Gln	Val Glu Lys Glu Glu	Thr		
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Pro Gln Glu Pro	Gly Arg Glu Gln Val	Val Glu Asp Arg Pro	Val		
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Gln Val Gln Ala	Ala Leu Ser Val Ser	Gln Glu Asn Pro Glu	Met		
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Glu Gly Pro Glu	Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln	Glu		
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Arg Gly Glu Asp	Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu	Ser		
	350		355		360
Glu Thr Asp Lys	Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn	Ile		
	365		370		375
Asp Val Phe Asn	Val Glu Asp Gln Lys	Arg Asp Thr Ile Asn	Leu		
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<212> DNA

<213> Homo sapiens

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<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	

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Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	200	205	210
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	215	220	225
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	230	235	240
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met	245	250	255
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Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	335	340	345
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala	350	355	360
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser	365	370	375
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	380	385	390
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	395	400	405
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Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	425	430	435
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	440	445	450

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Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	485	490	495
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Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	515	520	525
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Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	545	550	555
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Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	590	595	600
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His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	620	625	630
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Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	650	655	660
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	665	670	675
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	680	685	690
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Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	710	715	720
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	725	730	735

Val	Ser	Gly	Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu	740	745	750
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Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile	845	850	855
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Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr	890	895	900
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile	905	910	915
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser	920	925	930
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Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu	980	985	990
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Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu	1010	1015	1020

Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
				1025					1030					1035
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040					1045					1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
				1055					1060					1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val		95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro		110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu		125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile		140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr		155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile		170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys		185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys		200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val		215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro		230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu		245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser		260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys		275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys		290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser		305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu		320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp		335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro		350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr		365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
425 430 435

Leu Tyr Val Gln Met Glu Asn
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

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<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgcca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<223> Synthetic oligonucleotide probe

<400> 109
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<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

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tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150

gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

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ccccgactac caccatga cccacgcaa cgacatctgc ctgctgcggc 450

tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500

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<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

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Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly	50	55	60	
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys	65	70	75	
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala	80	85	90	
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile	95	100	105	
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala	110	115	120	
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly	125	130	135	
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro	140	145	150	
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val	155	160	165	
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val	170	175	180	
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His	185	190	195	
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg				

	200	205	210
Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg	215	220	225
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly	230	235	240
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val	245	250	255
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly	260	265	270
Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala	275	280	

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 112
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<210> 113
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<220>
 <223> Synthetic oligonucleotide probe

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 114
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<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

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<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	
				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155					160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	185	190	195
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	200	205	210
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	215	220	225
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	230	235	240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	245	250	255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	260	265	270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	275	280	285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	290	295	300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	305	310	315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	320	325	330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

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agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150
tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200
tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala
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Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr
				20					25				30	

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
				35					40				45	

Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala
				50					55				60	

Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu
				65					70				75	

His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe
				80					85				90	

Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His
				95					100				105	

Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr
				110					115				120	

Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly
				125					130				135	

Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn
				140					145				150	

Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser
				155					160				165	

Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr
				170					175				180	

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser	530	535	540

Ser Pro Glu Asp

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 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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 cgggacagga gaccagaaa ggg 23

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 122

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gaatcgggcc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200
cgcggggact cggagcaggt gcgctactgc gcgcgttct cctacctctg 250
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 catgttttgt tttgttttta aaaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
				20					25					30
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly

	170		175		180
Val Pro Tyr Thr	Cys Cys Ile Arg Asn	Thr Thr Glu Val Val	Asn		
	185		190		195
Thr Met Cys Gly	Tyr Lys Thr Ile Asp	Lys Glu Arg Phe Ser	Val		
	200		205		210
Gln Asp Val Ile	Tyr Val Arg Gly Cys	Thr Asn Ala Val Ile	Ile		
	215		220		225
Trp Phe Met Asp	Asn Tyr Thr Ile Met	Ala Cys Ile Leu Leu	Gly		
	230		235		240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu	Tyr		
	245		250		255
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr	Asp		
	260		265		270
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala	Gly		
	275		280		285
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn				
	290				

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

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Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu				

				170					175					180
Ala	Lys	Gln	Val	Met 185	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu 195
Val	Lys	Asn	Gln	Leu 200	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly 210
Met	Tyr	Ala	Asp	Leu 215	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu 225
Ser	Ile	Asp	Arg	Leu 230	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys 240
Gly	Asp	Thr	Ile	Gln 245	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser 255
Gln	Gly	Lys	Val	Thr 260	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu 270
Thr	Met	Pro	Thr	Leu 275	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser 285
Gln	Asp	Val	Val	Lys 290	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu 300
Glu	Phe	Met	Val	Leu 305	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His 315
Arg	Leu	Lys	Ser	Ser 320	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp 330
Lys	Leu	Gly	Ser	Thr 335	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr 345
Pro	Glu	Phe	Phe	Ile 350	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu 360
Ile	Val	Leu	Glu	Val 365	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu 375
Phe	Thr	Leu	Gly	Ile 380	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr 390
Lys	Gly	Asp	Gln	Leu 395	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp 405
Arg	Ile	Gln	Leu	Met 410	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp 420
Val	Leu	Lys	Asn	Ile 425	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu 435
Pro	Asn	Gln	Asn	Gly 440	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu 450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys

455	460	465
Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser		
470	475	480

Pro Val Ser Gln

<210> 129

<211> 2213

<212> DNA

<213> Homo sapiens

<400> 129

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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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	20	25	30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met	35	40	45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys	50	55	60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile	65	70	75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys	80	85	90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg	95	100	105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp	110	115	120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser	125	130	135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg	140	145	150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln	155	160	165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val	170	175	180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu	185	190	195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met	200	205	210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys	215	220	225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg	230	235	240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn	245	250	255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His	260	265	270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu	275	280	285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys	290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser			

	305		310		315
Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr					
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Ser Phe Leu Met Ser					
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<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
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 caatttggtt cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggc ctagatccaa attatacaac 450
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<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132

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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25					30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40					45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55					60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70					75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	

Tyr Ser Ser Tyr	Thr Lys Asn Cys Thr	Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn	Ile Arg Ala Phe Tyr	Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met	Leu Gly Glu Ile Ile	Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln	Lys Thr Ile Val Ile	Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met	Glu His Arg Gln Phe	Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala	His Val Pro Leu Leu	Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu	Gln Val Ser Asn Val	Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met	Leu Asp Ile Ala Gly	Ile Pro Leu Pro Gln Asn	365	370	375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	380	385	390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	395	400	405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	410	415	420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	425	430	435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	440	445	450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	455	460	465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	470	475	480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	485	490	495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	500	505	510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	515	520	525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val	530	535	

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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ctacatccta ggccttcttg ggcttttggg cacttggtt gccatgctgc 200
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gttggttctt ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
catcacccag tgtgacatct atagcacctt tctgggcctg ccgctgaca 350
tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctctccctg 400
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450
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<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
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 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly
 50 55 60
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
 65 70 75
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
 80 85 90
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
 95 100 105
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala
 110 115 120
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
 125 130 135
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
 140 145 150
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
 155 160 165
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
 170 175 180
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
 185 190 195
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
 200 205 210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
 215 220 225

Leu Thr Gly Tyr Val
 230

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 gattttgttg tgaagctgaa gggttcagggt gtgaattccc agtgccactc 350
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 agtccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

	65		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
				95					100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
				110					115					

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 138
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
 1 5 10 15

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				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
				35					40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
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<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

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				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
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Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ccttcctgcc ctcccttctc gccaccgct gcttctctggc 150
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 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgaact 250
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 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450
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 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
 tgggagaaag agaggcccg gcacccacgc cccactggc ctcagcgcgc 950
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 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
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tcggccccctt gccctgcac cttatgcacct gtgaggatgg ccgccaggac 1150
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 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
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<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro		125	130	135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys		140	145	150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro		155	160	165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu		170	175	180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg		185	190	195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly		200	205	210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe		215	220	225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val		230	235	240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly		245	250	255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg		260	265	270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly		275	280	285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys		290	295	300
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro		305	310	315
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg		320	325	330
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser		335	340	345
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala		350	355	360
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu		365	370	375
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His		380	385	390
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala		395	400	405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
 410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
 425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
 440 445 450

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

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cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150

tgggctacgc gtcctcggtt atcgtgaccc cgggagagcg gcggaagcag 200

gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250

ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300

cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350

ggcgccagcg ggaggtcacc gtgagaccgg acttgctctc gtgggcgcgg 400

gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500

gtgagctgcc gtccgggtgag caggtttccc ccaaaccctg gactgactgc 550

tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600

aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15

Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90

Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 caggctgcca tggggcccag caccctctc ctcactctgt tccttttgtc 150
 atggctcgga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
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 gagaccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
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 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
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 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
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 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
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 acgtccagct ctgtcctctc ttccctactc ctcccttcag tgtcctgagg 1750
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 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1					5				10					15

Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20				25						30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala
				260					265					270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala
				275					280					285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys
				290					295					300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro
				305					310					315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr
				320					325					330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile

	335		340		345
Gln Cys Ser Phe	Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg	Ala		
	350	355	360		
Ala Leu Pro Tyr	Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser	Leu		
	365	370	375		
Arg Tyr Asn Pro	Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp	Gly		
	380	385	390		
Tyr Gln Ile Val	Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu	Glu		
	395	400	405		

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
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 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttg 250
 gccagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctcct 300
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 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
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 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750
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 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850

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ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950
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aa 2052

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<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

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Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val Gln	Ala
	20	25	30
Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser Pro	Lys
	35	40	45
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly Gln	Phe
	50	55	60
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln Pro	Phe
	65	70	75
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val Lys	Asp
	80	85	90
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn Ile	Thr
	95	100	105
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser Gln	Ser
	110	115	120
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala Leu	Gly
	125	130	135
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg Asp	Ile
	140	145	150
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro Thr	Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp Ser	Arg
	170	175	180
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile Ser	Leu
	185	190	195
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met Arg	His
	200	205	210
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile Gly	Asp
	215	220	225
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys Val	Leu
	230	235	240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu	Lys
	245	250	255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu	Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys

290	295	300
Leu Cys Val Ser Asp 305	Leu Lys Thr Val Thr His Arg Lys Ala Pro 310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val 320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val 335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp 350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His 365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr 380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr 395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe 410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg 425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn 440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu 455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu 470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu 485	490	495
Pro Arg Gly Glu Met 500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 150

ggaactgacc cagtgtgac acc 23

<210> 151

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 151

gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152

<211> 2294

<212> DNA

<213> Homo sapiens

<400> 152

gcgatggtgc gcccggtggc ggtggcgggc gcggttgccg aggcctcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgcgcgcg ccgcccgcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggcggcggc ggggcccgcg ggacggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac ccctcccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggccc ccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400
caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
tggcccgccg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgcggccag gttatcaggg gcttcactgt 800

gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaacaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacaaggaggatga 1000
gggtcataga ttacaaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
atctcatggg aaaaaattat tgaagaataa atctgcttct tggaagggct 1200
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250
atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatttaac tagtggttaag tagactggtt ttactctatt 1400
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaaat ctagtggaaat aatgtactgt 1500
tatctaagca ttgacctgt actgcactga aagtaattat tctttgacct 1550
tatgtgaggc acttggttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataatgaaaa aaataatgac aggttatact cagtgttaacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750
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ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850
tgttttaaga acttttagct ctttgacaaa gaagtgttt atactttagc 1900
actaaatatt ttaaatgctt tataaatgat attatactgt tatggaatat 1950
tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
ctcacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050
tgaggccagg agttctagat gagcctggcc agcacagtga aacccgtct 2100
ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150
tcccagctac tcgggaggct gaggcaggag aatcggttga acccgaggag 2200

tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250

agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180
Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195
Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210
Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225
Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255

Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 154

aactgctctg tggttggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157

<211> 689

<212> DNA

<213> Homo sapiens

<400> 157

tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50

ttctggcttt ggtctcggtg ccagggccc aggcctgtgt gttgggaaga 100

ctggaccctg agcagcttct tgggcccttg tacgtgcttg cggtggcctc 150

ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200

tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250

cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcca tcattttcac tcagctggag 400
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
 gggtcctgtg acctcgcca gtgtccaccc acctcgctca gcggtcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

Met	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Phe	Leu	Ala	Leu	Val	Ser	Val	1	5	10	15
Pro	Arg	Ala	Gln	Ala	Val	Trp	Leu	Gly	Arg	Leu	Asp	Pro	Glu	Gln	20	25	30	
Leu	Leu	Gly	Pro	Trp	Tyr	Val	Leu	Ala	Val	Ala	Ser	Arg	Glu	Lys	35	40	45	
Gly	Phe	Ala	Met	Glu	Lys	Asp	Met	Lys	Asn	Val	Val	Gly	Val	Val	50	55	60	
Val	Thr	Leu	Thr	Pro	Glu	Asn	Asn	Leu	Arg	Thr	Leu	Ser	Ser	Gln	65	70	75	
His	Gly	Leu	Gly	Gly	Cys	Asp	Gln	Ser	Val	Met	Asp	Leu	Ile	Lys	80	85	90	
Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu	95	100	105	
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile	110	115	120	
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu	125	130	135	
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu	140	145	150	
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln	155	160				

<210> 159

<211> 1665
<212> DNA
<213> Homo sapiens

<400> 159
aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg cccctgctct gggggagggg gagggcgga ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cggtcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttacc 200
tggcccagta gttcatggct actggttccg ggaaggggccc aatacagacc 250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggataggag ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950
ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
ctgcagagca aagccacatc aggagtgact cagggggtgg tcgggggagc 1100
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctacggggcc 1250
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

ettctgcccc ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttccaga tggatgaagcc ttgggactcg cggggacagg aggccactga 1400
 caccgagtag tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	
1				5					10					15	
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	
				20					25					30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	
				35					40					45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	
				50					55					60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	
				65					70					75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	
				80					85					90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	
				95					100					105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	
				110					115					120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	
				125					130					135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	
				140					145					150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	
				155					160					165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	
				170					175					180	

Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg Ser
185	190	195
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr Ser
200	205	210
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr Asn
215	220	225
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu Thr
230	235	240
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu Gly
245	250	255
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg Leu
260	265	270
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg Leu
275	280	285
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro Ser
290	295	300
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp Ala
305	310	315
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln Gln
320	325	330
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly Val
335	340	345
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val Phe
350	355	360
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg Lys
365	370	375
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile Glu
380	385	390
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu Thr
395	400	405
Glu Pro Trp Ala	Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro Ala
410	415	420
Ser Ala Arg Ser	Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala Ser
425	430	435
Leu Ser Phe Gln	Met Val Lys Pro Trp	Asp Ser Arg Gly Gln Glu
440	445	450
Ala Thr Asp Thr	Glu Tyr Ser Glu Ile	Lys Ile His Arg
455	460	

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161
gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250
gagggaggat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
acacagagcc cggaccacct ggacctacc tccagccatg acccttccct 650
gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15
Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
20 25 30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
35 40 45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
50 55 60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
65 70 75

Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	80	85	90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	95	100	105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	110	115	120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	125	130	135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	140	145	150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	155	160	165
Cys	Val	Pro	Glu	His											170		

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 165
 gtcctccgga aagtccttat c 21

<210> 166
 <211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
cagggacctg gtacgtgaag gccatgggtg tcgataagga cttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
gttccgcaga tgcagagggt gaggtggctg cgggactgga agtcatcggt 50
cagaggtctc acagcagcca aggaacctgg ggcccgtctc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtggg 250
cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggagg 350
ctgtgagcag acccgacag ccactgagtc cttccccac cccggcttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500

ctcacgctgt gtcaactgctg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag cccccagtta cgcctgcctc acaccttgcg atgcgccaac 600
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
 attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggaccacc caccacagcc catcacctc catttccact 900
 tgggtgtttgg ttctgttca ctctgttaat aagaaaccct aagccaagac 950
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100
 tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
 1 5 10 15
 Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
 20 25 30
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
 35 40 45
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
 50 55 60
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 65 70 75
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
 80 85 90
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
 95 100 105

Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
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<210> 171
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 171
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<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 172
 ctccaggcca tgaggattct gcag 24

<210> 173
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
cctctgggtct gtaaccag 18

<210> 174
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
cgtgtagaca ccaggctttc gggcg 25

<210> 176
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 176
cccttgatga tcctgggc 18

<210> 177
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<212> DNA
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<220>
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<400> 177
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<213> Artificial Sequence

<220>
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<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
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agaaaactgc tctaagacaa gcaagaaggg agacctaata aatgccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
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aaaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
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Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	155	160	165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	170	175	180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	200	205	210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				215	220	

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 183
cctttcagga tgtaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
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<400> 185
gcatcctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 187

gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

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cccaaagtct tcctgtgtca ataactca ctgcacctgc aaccatggat 150

atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

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ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

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20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
agggaccatt gcttctttcca ggcc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cctgtgctaa gtgcccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
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gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
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cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

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<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
      20              25              30

Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
      35              40              45

Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
      50              55              60

Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
      65              70              75

Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
      80              85              90

Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
      95              100             105

Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
      110             115             120

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Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	
				125					130					135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	
				140					145					150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	
				155					160					165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	
				170					175					180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	
				185					190					195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	
				200					205					210	
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	
				215					220					225	
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	
				230					235					240	
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn								
				245											

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 <212> DNA
 <213> Homo sapiens

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 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

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Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
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<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

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Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro
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Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg
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Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu
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His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe
				95					100					105
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys
				110					115					120
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu
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Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg
				140					145					150
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp
				155					160					165
Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu
				170					175					180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg
				185					190					195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu
				200					205					210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp
				215					220					225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr
				230					235					240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp
				245					250					255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro
				260					265					270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr
				275					280					285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu
				290					295					300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu
				305					310					315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr

	320		325		330
Lys Lys Leu Lys Arg Ile Asp Ile Ser	335	Lys Asn Gln Ile Ser Asp	340		345
Ile Ala Pro Asp Ala Phe Gln Gly Leu	350	Lys Ser Leu Thr Ser Leu	355		360
Val Leu Tyr Gly Asn Lys Ile Thr Glu	365	Ile Ala Lys Gly Leu Phe	370		375
Asp Gly Leu Val Ser Leu Gln Leu Leu	380	Leu Leu Asn Ala Asn Lys	385		390
Ile Asn Cys Leu Arg Val Asn Thr Phe	395	Gln Asp Leu Gln Asn Leu	400		405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys	410	Leu Gln Thr Ile Ser Lys	415		420
Gly Leu Phe Ala Pro Leu Gln Ser Ile	425	Gln Thr Leu His Leu Ala	430		435
Gln Asn Pro Phe Val Cys Asp Cys His	440	Leu Lys Trp Leu Ala Asp	445		450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr	455	Ser Gly Ala Arg Cys Ser	460		465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	470	Ile Ser Gln Ile Lys Ser	475		480
Lys Lys Phe Arg Cys Ser Gly Ser Glu	485	Asp Tyr Arg Ser Arg Phe	490		495
Ser Ser Glu Cys Phe Met Asp Leu Val	500	Cys Pro Glu Lys Cys Arg	505		510
Cys Glu Gly Thr Ile Val Asp Cys Ser	515	Asn Gln Lys Leu Val Arg	520		525
Ile Pro Ser His Leu Pro Glu Tyr Val	530	Thr Asp Leu Arg Leu Asn	535		540
Asp Asn Glu Val Ser Val Leu Glu Ala	545	Thr Gly Ile Phe Lys Lys	550		555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	560	Ser Asn Asn Lys Ile Lys	565		570
Glu Val Arg Glu Gly Ala Phe Asp Gly	575	Ala Ala Ser Val Gln Glu	580		585
Leu Met Leu Thr Gly Asn Gln Leu Glu	590	Thr Val His Gly Arg Val	595		600
Phe Arg Gly Leu Ser Gly Leu Lys Thr		Leu Met Leu Arg Ser Asn			

	605		610		615
Leu Ile Ser Cys	Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser	Ser		
	620		625		630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile	Thr		
	635		640		645
Pro Gly Ala Phe	Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn	Leu		
	650		655		660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys	His Leu Ala Trp Leu	Gly		
	665		670		675
Lys Trp Leu Arg	Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg	Cys		
	680		685		690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val	Ala		
	695		700		705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys	Gln		
	710		715		720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr	Val		
	725		730		735
Val Arg Cys Ser	Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly	Met		
	740		745		750
Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu	Thr		
	755		760		765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu	Ile		
	770		775		780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr	Phe		
	785		790		795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn	Arg		
	800		805		810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser	Leu		
	815		820		825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro	Glu		
	830		835		840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu	Gly		
	845		850		855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser	Glu		
	860		865		870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys	Ser		
	875		880		885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro	Thr		

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His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala					
				905					910					915					
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr					
				920					925					930					
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr					
				935					940					945					
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile					
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Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser					
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His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly					
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Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys					
				995					1000					1005					
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys					
				1010					1015					1020					
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile					
				1025					1030					1035					
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys					
				1040					1045					1050					
Cys	Ile	Pro	Leu	Asp	Lys	Gly	Phe	Ser	Cys	Glu	Cys	Val	Pro	Gly					
				1055					1060					1065					
Tyr	Ser	Gly	Lys	Leu	Cys	Glu	Thr	Asp	Asn	Asp	Asp	Cys	Val	Ala					
				1070					1075					1080					
His	Lys	Cys	Arg	His	Gly	Ala	Gln	Cys	Val	Asp	Thr	Ile	Asn	Gly					
				1085					1090					1095					
Tyr	Thr	Cys	Thr	Cys	Pro	Gln	Gly	Phe	Ser	Gly	Pro	Phe	Cys	Glu					
				1100					1105					1110					
His	Pro	Pro	Pro	Met	Val	Leu	Leu	Gln	Thr	Ser	Pro	Cys	Asp	Gln					
				1115					1120					1125					
Tyr	Glu	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Val	Gln	Gln	Glu					
				1130					1135					1140					
Pro	Thr	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ala	Gly	Pro	Arg	Cys	Glu					
				1145					1150					1155					
Lys	Leu	Ile	Thr	Val	Asn	Phe	Val	Gly	Lys	Asp	Ser	Tyr	Val	Glu					
				1160					1165					1170					
Leu	Ala	Ser	Ala	Lys	Val	Arg	Pro	Gln	Ala	Asn	Ile	Ser	Leu	Gln					

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
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Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

<210> 199

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 200

ttgttggcat tgaggaggag cagc 24

<210> 201

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 201

gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202

<211> 753

<212> DNA

<213> Homo sapiens

<400> 202

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gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
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gtc 753

<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
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Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
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<210> 204

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<223> Synthetic oligonucleotide probe

<400> 204

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<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

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<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
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 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp				

	155		160		165
Trp Glu Arg Val	His Leu Ile Val Ala	Gly Gly Tyr Asp Glu Arg			
	170	175			180
Val Leu Glu Asn	Val Glu His Tyr Gln	Glu Leu Lys Lys Met Val			
	185	190			195
Gln Gln Ser Asp	Leu Gly Gln Tyr Val	Thr Phe Leu Arg Ser Phe			
	200	205			210
Ser Asp Lys Gln	Lys Ile Ser Leu Leu	His Ser Cys Thr Cys Val			
	215	220			225
Leu Tyr Thr Pro	Ser Asn Glu His Phe	Gly Ile Val Pro Leu Glu			
	230	235			240
Ala Met Tyr Met	Gln Cys Pro Val Ile	Ala Val Asn Ser Gly Gly			
	245	250			255
Pro Leu Glu Ser	Ile Asp His Ser Val	Thr Gly Phe Leu Cys Glu			
	260	265			270
Pro Asp Pro Val	His Phe Ser Glu Ala	Ile Glu Lys Phe Ile Arg			
	275	280			285
Glu Pro Ser Leu	Lys Ala Thr Met Gly	Leu Ala Gly Arg Ala Arg			
	290	295			300
Val Lys Glu Lys	Phe Ser Pro Glu Ala	Phe Thr Glu Gln Leu Tyr			
	305	310			315
Arg Tyr Val Thr	Lys Leu Leu Val				
	320				

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccg atccgagacg tggctccctg gccggcagaa ccatgttgga 50
 cttcgcgata ttcgccgtta ccttcttgct gccgttggtg ggagccgtgc 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgggaag 200
 tttgcatgag ttctgtggtta atttgcatga gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctcgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000
 ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	
				20					25					30	
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	
				35					40					45	
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	
				50					55					60	
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	
				65					70					75	
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	
				80					85					90	
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	
				95					100					105	
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	
				110					115					120	
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	
				125					130					135	
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	
				140					145					150	
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser	
				155					160					165	
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val	
				170					175					180	
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln	
				185					190					195	
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu	
				200					205					210	
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu	
				215					220					225	
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys	
				230					235					240	
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser	
				245					250					255	
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser	
				260					265					270	
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	
				275					280					285	
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	
				290					295					300	

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305					310					315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320					325					330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335					340					345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350					355					360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365					370					375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380					385					390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395					400					405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410					415					420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425					430					435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440					445					450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455					460						

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
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 tccagcctca gagaccgcg cccttgctcc cgagggccat gggccgggtc 100
 tcagggttg tgccctctcg cttcctgacg ctctggcgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt caccctcgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctocattg 350
 gggctcactg tagtgcatcc gtggccctgt cttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacatTTTT gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750
aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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cctgggctct cccagcctc cttcgactcg gagcggctca ggagacagaa 100
 gacccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggtac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
 ccaggccatc cgggcagccc agggctctact ggcctgcggg gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctaccgctcc cctgagggcc ctgctgatcc gcacccatt cctcccctcc 650
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1				5					10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
			20						25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
			35						40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
			50						55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
			65						70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
			80						85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
			95						100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
			110						115					120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	
				125					130					135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	
				140					145					150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	
				155					160					165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	
				170					175					180	
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser	
				185					190					195	

Pro

<210> 217
 <211> 1871
 <212> DNA
 <213> Homo sapiens

<400> 217
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 gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
 tctatctggt catctgtggc caggatgatg gtccctcccg ctcagaggac 150
 cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcgga 200
 gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacggggcc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
 ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700
 tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggctg 750
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacaccggg caggggaagg 900
 gttgggcctc aggcaggag gaggggtggag acgaggagat gccaaagtgg 950
 gccagggccca agtctcaagt ggcagagaaa ggggcccaag tgctgggtccc 1000
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
 gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
 gcaacagggg gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
 atggatggct gagagggtt cctaggagcc agtcagcagg gtgggggtgg 1300
 gccagaggag ctctccagcc ctgcctagtg ggcgccctga gccccttgtc 1350
 gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
 ttcctcttcc tgccagtact cccctgtac caccattgc tgatggcaca 1500
 cccatcctta agctaagaca ggacgattgt ggtcctccca cactaaggcc 1550
 acagcccatc cgcgtgctgt gtgtccctct tccaccccaa ccctgctgg 1600
 ctctcttggg agcatccatg tcccggagag gggccctca acagtcagcc 1650
 tcacctgtca gaccgggggt ctcccggatc tggatggcgc cgcctctca 1700
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 tgttctgtgt gtctgtctgt ggggtggggg aggggaggga agtcttgtga 1800
 aaccgtgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
 aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
1				5					10					15

Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20					25					30

Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	215	220	225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	230	235	240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				245	250	

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150

agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200

gcgcgcgcgc cgccgtcgct cctgcagcgc tgtcgacctc gccgctagca 250
tcttccccgag caccgggcatc ccggggtagg aggcgacgcg ggcgagcacc 300
agcgccagcc ggctgcggtc gccacacgcg ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcgggtgc cggccgtgct gctggctctc acgctgccgg 400
ggctgcccgt ctgggcacag aacgacacgc agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgca ctggaacccg gccacggact ccaagggctc 500
ctcttctctc ccgctgggga tatcggtccg ggccggccaac tccaaggctc 550
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgatcagatc ctgggtgaatg tgggtaattt 650
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800
tggtactcgt gaagctgcc cgaatggtgt cctgctctac ctagataaag 850
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cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg ttttttattg gtttctcatg 1050
ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100
tcacagatta tttgtgtgtg tctgtttcag tatatttggg ttgggactct 1150
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
gaattttatt tgttttagttt taaaagactg gcaaccaggt ctaaggatta 1300
gaaaactcta aagttctgac ttcaatcaac ggtagtggtg atactgccaa 1350
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400
ggaattagtt tgtttgggtc ttgtaaaaaa cttggatttt ttttttcagt 1450
aactggtatt atgttttctc ttaaaataag gtaatgaatg gcttgccac 1500
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600
ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgtcga atccctgagc ctcagcaaaa 1700
 cagctcccct ccgagggaaa tcttatactt tattgtctcaa ctttaattaa 1750
 aatgattgat aataaccact ttattaaaaa cctaagggtt tttttttttc 1800
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900
 tgccttaact ctttaaattg tatatatatta tctgttttagc taatattaaa 1950
 ttcaaataat ccataatctaa atttagtgca atatcttgct ttttgtatag 2000
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<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu	1	5	10	15
Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp	20	25	30	
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp	35	40	45	
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu	50	55	60	
Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	65	70	75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	80	85	90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	95	100	105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	110	115	120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	125	130	135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	140	145	150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	155	160	165	

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
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Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
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Phe Leu Val Phe Pro Leu
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<212> DNA
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<400> 222
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<210> 223
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<212> DNA
<213> Artificial Sequence

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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

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<211> 257
<212> PRT
<213> Homo sapiens
<400> 225

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35 40 45
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
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80 85 90
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
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 <211> 3939
 <212> DNA
 <213> Homo sapiens
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Ser Arg

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser 110
 Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn 125
 Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly 140
 Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val 155
 Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly 170
 Cys Glu Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr 185
 His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly 200
 Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr 215
 Trp Ala Phe Leu Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu 230
 Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg 245
 255

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<211> 832
<212> PRT
<213> Homo sapiens

<400> 227
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Lys Asp Ala Gln Phe Gln Arg Thr Tyr Val Asp Gln Val Asn Ser
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40
45
Gln Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
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55
60
Arg Thr Gln Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
65
70
75
Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Gln Ala Val
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Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
95
100
105
Lys Tyr Leu Tyr Gln Lys Val Gln Arg Thr Leu Cys Gln Pro
110
115
120
Thr Lys Asn Gln Ser Gln Ile Gln Phe Phe Tyr Val Asp Val Ser

125	130	135	Thr Leu Ser Pro Val Asn Thr Tyr Gln Leu Arg Val Ser Arg
140	145	150	Met Asp Asp Phe Val Leu Arg Thr Gly Gln Phe Ser Phe Asn
155	160	165	Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Gln Phe Pro Gln
170	175	180	Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
185	190	195	Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
200	205	210	Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
215	220	225	Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
230	235	240	Asn Ser Phe Tyr Val Val Val Val Lys Thr Gln Asp Gln Ala
245	250	255	Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Gln Asp Gln Pro
260	265	270	Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
275	280	285	Gln Ala Val Thr Ser Gln Ala Tyr Val Ser Gly Met Leu Phe Cys
290	295	300	Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
305	310	315	Cys Trp Gln Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala
320	325	330	Ile Asp Arg Ala Cys Pro Gln Ser Gly His Pro Arg Val Leu Ala
335	340	345	Asp Ser Phe Pro Gly Ser Ser Pro Tyr Gln Gly Tyr Asn Tyr Gly
350	355	360	Ser Phe Gln Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser
365	370	375	Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe
380	385	390	Gln Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val
395	400	405	Gln Gln Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys

420	415	410	Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala
435	430	425	Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe
450	445	440	Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val
465	460	455	Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn
480	475	470	Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly
495	490	485	Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile
510	505	500	Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Gln Ile
525	520	515	Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Gln
540	535	530	Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
555	550	545	Ala Leu Met Met Gln Gly Leu Leu Ser Ala Cys Tyr His Val Cys
570	565	560	Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met
585	580	575	Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro
600	595	590	Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile
615	610	605	Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn
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645	640	635	Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu
660	655	650	Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
675	670	665	Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
690	685	680	Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr

695 700 705

Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala 710 715 720

Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile 725 730 735

Met Lys Leu Arg Ser Gly Gln Arg Ile Lys Leu Ile Pro Leu Leu 740 745 750

Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe 755 760 765

Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Gln Ser 770 775 780

Arg Gln His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp 785 790 795

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser 800 805 810

Phe Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln 815 820 825

Arg Asp Lys Ile Tyr Val Phe 830

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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<211> 807
<212> PRT
<213> Homo sapiens

<400> 229
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Leu Pro Arg Gln Gly Ala Gln Gly Ile Val Leu Ser Gly Asp 50
Ser Gly Lys Ala Thr Gln Gly Pro Phe Ala Met Asp Pro Asp Ser 65
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Gln Gln Ala 75

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Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
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Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
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Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
				320					325					330					
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					

					365						370					375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala		
				380					385					390		
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu		
				395					400					405		
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met		
				410					415					420		
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val		
				425					430					435		
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile		
				440					445					450		
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro		
				455					460					465		
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu		
				470					475					480		
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr		
				485					490					495		
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val		
				500					505					510		
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser		
				515					520					525		
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly		
				530					535					540		
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val		
				545					550					555		
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu		
				560					565					570		
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr		
				575					580					585		
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu		
				590					595					600		
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly		
				605					610					615		
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp		
				620					625					630		
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu		
				635					640					645		
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His		

	650	655	660
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser
	665	670	675
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val
	680	685	690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr
	695	700	705
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile
	710	715	720
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val
	725	730	735
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg
	740	745	750
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val
	755	760	765
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile
	770	775	780
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp
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<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

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<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aacccctc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttcctgag 250
atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn	20	25	30	
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	
Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195	

Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	
				200					205					210	
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	
				215					220					225	
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	
				230					235					240	
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	
				245					250					255	
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	
				260					265					270	
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	
				275					280					285	
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	
				290					295					300	
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	
				305					310					315	
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	
				320					325					330	
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	
				335					340					345	
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	
				350					355					360	
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	
				365					370					375	
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	
				380					385					390	
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	
				395					400					405	
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	
				410					415					420	

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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tggtccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100

ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150
cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
aacaccgact ttgccttccg cctataccgc aggettggtt tggagacccc 250
gagtcagaac atctttcttct cccctgtgag tgtctccact tccctggcca 300
tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350
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ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgacctga 450
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agaagaccca agggaagggt gtagacataa tccaaggcct tgaccttctg 650
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gccctttcac cttgaatata caagaaagaa cttcccatc ctggtgggcg 750
agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800
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ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000
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tgacccagct ggagctggat tcgctggcag ggatgccact tccaaggctc 1450
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ccccagtcag tgcccttttc cacaaattct ccagagtaac tagcttcatg 1550
ggatgttgct gggttaccat atttccattc cttggggctc ccaggaatgg 1600
aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac 1650
attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

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<210> 236
<211> 417
<212> PRT
<213> Homo sapiens

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<400> 236
Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
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Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
              20              25              30

Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
              35              40              45

Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
              50              55              60

Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
              65              70              75

Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
              80              85              90

Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
              95              100             105

Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
              110             115             120

Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
              125             130             135

Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
              140             145             150

Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
              155             160             165

Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
              170             175             180

Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
              185             190             195

Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
              200             205             210

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Lys	Trp	Glu	Lys	Pro	Phe	His	Leu	Glu	Tyr	Thr	Arg	Lys	Asn	Phe	
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Pro	Phe	Leu	Val	Gly	Glu	Gln	Val	Thr	Val	Gln	Val	Pro	Met	Met	
				230					235					240	
His	Gln	Lys	Glu	Gln	Phe	Ala	Phe	Gly	Val	Asp	Thr	Glu	Leu	Asn	
				245					250					255	
Cys	Phe	Val	Leu	Gln	Met	Asp	Tyr	Lys	Gly	Asp	Ala	Val	Ala	Phe	
				260					265					270	
Phe	Val	Leu	Pro	Ser	Lys	Gly	Lys	Met	Arg	Gln	Leu	Glu	Gln	Ala	
				275					280					285	
Leu	Ser	Ala	Arg	Thr	Leu	Ile	Lys	Trp	Ser	His	Ser	Leu	Gln	Lys	
				290					295					300	
Arg	Trp	Ile	Glu	Val	Phe	Ile	Pro	Arg	Phe	Ser	Ile	Ser	Ala	Ser	
				305					310					315	
Tyr	Asn	Leu	Glu	Thr	Ile	Leu	Pro	Lys	Met	Gly	Ile	Gln	Asn	Ala	
				320					325					330	
Phe	Asp	Lys	Asn	Ala	Asp	Phe	Ser	Gly	Ile	Ala	Lys	Arg	Asp	Ser	
				335					340					345	
Leu	Gln	Val	Ser	Lys	Ala	Thr	His	Lys	Ala	Val	Leu	Asp	Val	Ser	
				350					355					360	
Glu	Glu	Gly	Thr	Glu	Ala	Thr	Ala	Ala	Thr	Thr	Thr	Lys	Phe	Ile	
				365					370					375	
Val	Arg	Ser	Lys	Asp	Gly	Pro	Ser	Tyr	Phe	Thr	Val	Ser	Phe	Asn	
				380					385					390	
Arg	Thr	Phe	Leu	Met	Met	Ile	Thr	Asn	Lys	Ala	Thr	Asp	Gly	Ile	
				395					400					405	
Leu	Phe	Leu	Gly	Lys	Val	Glu	Asn	Pro	Thr	Lys	Ser				
				410					415						

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

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<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggctctgtg ctccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

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<223> Synthetic oligonucleotide probe

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<210> 241

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<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300
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<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75
Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	365	370	375
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	380	385	390

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala	
				395					400					405	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				410					415					420	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Glu	Ala	Ser	Thr	Ala	
				425					430					435	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				440					445					450	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				455					460					465	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ala	Gly	Ser	Gly	Thr	Ala	
				470					475					480	
Ala	Leu	Thr	Gly	Met	His	Thr	Thr	Ser	His	Ser	Ala	Ser	Thr	Ala	
				485					490					495	
Val	Ser	Glu	Ala	Lys	Pro	Gly	Gly	Ser	Leu	Val	Pro	Trp	Glu	Ile	
				500					505					510	
Phe	Leu	Ile	Thr	Leu	Val	Ser	Val	Val	Ala	Ala	Val	Gly	Leu	Phe	
				515					520					525	
Ala	Gly	Leu	Phe	Phe	Cys	Val	Arg	Asn	Ser	Leu	Ser	Leu	Arg	Asn	
				530					535					540	
Thr	Phe	Asn	Thr	Ala	Val	Tyr	His	Pro	His	Gly	Leu	Asn	His	Gly	
				545					550					555	
Leu	Gly	Pro	Gly	Pro	Gly	Gly	Asn	His	Gly	Ala	Pro	His	Arg	Pro	
				560					565					570	
Arg	Trp	Ser	Pro	Asn	Trp	Phe	Trp	Arg	Arg	Pro	Val	Ser	Ser	Ile	
				575					580					585	
Ala	Met	Glu	Met	Ser	Gly	Arg	Asn	Ser	Gly	Pro					
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<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150
ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300
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tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400
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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	
Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser	185	190	195	
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser	200	205	210	
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly				

	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240
Ser Val Ala Asn Ile Met Pro			
	245		

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 249
 caatatgcat cttgcacgtc tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 251
 tgacccatt gagaagggtca ttgaagggat caaccgaggg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

<400> 252
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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile	
				125					130					135	
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly	
				140					145					150	
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn	
				155					160					165	
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp	
				170					175					180	
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala	
				185					190					195	
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe	
				200					205					210	
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro	
				215					220					225	
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe	
				230					235					240	
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	
				245					250					255	
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	
				260					265					270	
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	
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Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	
				290					295					300	
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	
				305					310					315	
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	
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Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	
				335					340					345	
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	
				350					355					360	
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys	
				365					370					375	
Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro	
				380					385					390	
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	
				395					400					405	

Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val
	665	670	675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro
	680	685	690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
				695					700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
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Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
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Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
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Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
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Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
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Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
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Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
				800					805					810	
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
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 <213> Artificial Sequence

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 <223> Synthetic oligonucleotide probe

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<220>
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 <222> 3635
 <223> unknown base

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 agggcgggac gggagcccg actcgtctgc cgccgccgtc gtcgccgtcg 150

 tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200

 cgcccagacc gccgctagcg cgccgccggc atggtcccct cttaaaggcg 250

 caggccgcgg cggcgggggc ggggtgtgcg aacaaagcgc cggcgcgggg 300

 cctgcggggc gctcgggggc cgcgatgggc gcggcgggcc cgcggcggcg 350

 gcggcgctgc ccgggccggg cctcgcggcg ctagggcggg ctggcctccg 400

 tgggcggggg cagcgggctg agggcgcgcg gaggcctgcg cggcggcggc 450

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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	
				20					25					30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
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Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	
				245					250					255	
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	
				260					265					270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	

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Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala					
				290					295					300					
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu					
				305					310					315					
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg					
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Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser					
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Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro					
				350					355					360					
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu					
				365					370					375					
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly					
				380					385					390					
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu					
				395					400					405					
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala					
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Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly					
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Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp					
				440					445					450					
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val					
				455					460					465					
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile					
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Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys					
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Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser					
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Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu					
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His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu					
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Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu					
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Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu					

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Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
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Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
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				620					625					630					
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg					
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Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe					
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
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Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn					
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Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
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Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
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Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
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Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
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Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
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Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
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Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 263
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<212> DNA
<213> Homo sapiens

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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90

Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly	95	100	105
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro	110	115	120
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala	125	130	135
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu	140	145	150
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val	155	160	165
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro	170	175	180
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu	185	190	195
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys	200	205	210
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp	215	220	225
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala	230	235	240
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu	245	250	255
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala	260	265	270
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro	275	280	285
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile	290	295	300
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp	305	310	315
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val	320	325	330
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala	335	340	345
Leu	Leu	Lys	Val	Tyr											350		

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20				25					30	

Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
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35					40					45				
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr
				95					100					105
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile
				110					115					120
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly
				125					130					135
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile
				140					145					150
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg
				170					175					180
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile
				185					190					195
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu
				200					205					210
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu
				215					220					225
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu
				230					235					240
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile
				245					250					255
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val

	320		325		330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val	335		340		345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp	350		355		360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn	365		370		375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr	380		385		390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr	395		400		405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe	410		415		420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys	425		430		435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr	440		445		450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp	455		460		465

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<210> 268

<211> 2103

<212> DNA

<213> Homo sapiens

<400> 268

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<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269
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35 40 45
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210

Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
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Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	
				230					235					240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	
				245					250					255	
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	
				260					265					270	
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	
				275					280					285	
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	
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Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	
				305					310					315	
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	
				320					325					330	
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	
				335					340					345	
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	
				350					355					360	
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	
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Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	
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Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	
				395					400					405	
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<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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				20					25					30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35					40					45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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<212> PRT

<213> Homo sapiens

<400> 273

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Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu	35	40	45	
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe	50	55	60	
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile	65	70	75	
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu	80	85	90	
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys	95	100	105	
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met	110	115	120	

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	
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Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	
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Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	
				155					160					165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	
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Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
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Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
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Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
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Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
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Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
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Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
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<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
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Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
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Cys Phe Arg Lys	His	Thr Asp Val Phe	Asn Trp Lys Val Arg	Ala
	245		250	255
Gly Ser Asp Lys	Leu	Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
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Ile Ile Ile Ile	Glu	Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
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Ile Ala Leu Met	Lys	Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
	290		295	300
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Gly Gly Lys Met	Ser	Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
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Ile Asp Ser Thr	Arg	Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
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Val Thr Glu Lys	Met	Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
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Asp Thr Cys Gln	Gly	Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
	380		385	390
Asp Gln Trp His	Val	Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
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Gly Gly Pro Ser	Thr	Pro Gly Val Tyr	Thr Lys Val Ser Ala	Tyr
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<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
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Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
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Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val	410	415	420
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr	425	430	435
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly	440	445	450
Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp	455	460	465
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala	470	475	480

Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala	485	490	495
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg	500	505	510
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu	515	520	525
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg	530	535	540
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser	545	550	555
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala	560	565	570
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala	575	580	585
Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	590	595	600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	605	610	615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	740	745	750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala					755	760	

<210> 278
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 278
ctgctggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
aggggtccctt agccgggcgc agggcgcgca gcccaggctg agatccgcgg 50
cttcgtaga agtgagcatg gctgggcagc gaggcttct tctagtgggc 100
ttccttctcc ctggggtcct gctctcagag gctgccaaaa tcctgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450

ggatatcatg gattccttaa agaattgagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600
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 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200
 gtccctgtct ctggtgcccc cagtgaagctc cttcttggtg gagcaggcat 2250
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 tctctcccca acctcactaa 2320

<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile

155										160					165				
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro					
				170					175					180					
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met					
				185					190					195					
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe					
				200					205					210					
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile					
				215					220					225					
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu					
				230					235					240					
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe					
				245					250					255					
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly					
				260					265					270					
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn					
				275					280					285					
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu					
				290					295					300					
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu					
				305					310					315					
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys					
				320					325					330					
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn					
				335					340					345					
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His					
				350					355					360					
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile					
				365					370					375					
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu					
				380					385					390					
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys					
				395					400					405					
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu					
				410					415					420					
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser					
				425					430					435					
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser					

	440		445		450
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr					
	455		460		465
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp					
	470		475		480
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu					
	485		490		495
Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala					
	500		505		510
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr					
	515		520		

<210> 283

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 283

tgccctttgct cacctacccc aagg 24

<210> 284

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 284

tcaggctggt ctccaaagag aggg 24

<210> 285

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 285

cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 286

gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50

ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
ccaggagagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450
gggttgaga gccctcagc catgttggga gccaaagccac actggctacc 500
aggtccccta cacagtcccg ggctgccctt ggttctgggtg cttctggccc 550
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tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
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accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
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 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
			20						25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
			35						40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
			50						55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
			65						70					75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 289
 cagagagga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 290

ctgtgctact gcccttgga cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50

tagccgcca gcctcgacgc cgtcccgga ccctgtgct ctgcgcgaag 100

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ttccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200

ccgcctactc cggggctctg cgcggcgagc gtcaggccga ggctgaccgg 250

agccagcgt ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300

atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350

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gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800

agtacctgat gtctggaggt atctgcctg tcagccggga caccatagac 850

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acattggttt cgccccatgc atcttccatg gtcgaggcct cttctcctcc 1150

gacacctggg ggctgggtgc ctactccaag cccatcacca ctgttgaggg 1200

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 tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttaaaa 1450
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<210> 292

<211> 388

<212> PRT

<213> Homo sapiens

<400> 292

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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	

Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly	260	265	270
Ala	Asp	Leu	Val	Pro	Ile	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr	275	280	285
Lys	Gln	Val	Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Gln	290	295	300
Lys	Lys	Phe	Gln	Lys	Tyr	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His	305	310	315
Gly	Arg	Gly	Leu	Phe	Ser	Ser	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr	320	325	330
Ser	Lys	Pro	Ile	Thr	Thr	Val	Val	Gly	Glu	Pro	Ile	Thr	Ile	Pro	335	340	345
Lys	Leu	Glu	His	Pro	Thr	Gln	Gln	Asp	Ile	Asp	Leu	Tyr	His	Thr	350	355	360
Met	Tyr	Met	Glu	Ala	Leu	Val	Lys	Leu	Phe	Asp	Lys	His	Lys	Thr	365	370	375
Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val	Leu	Glu	Val	Asn			380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

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ccgacgcagg gccggggccg gccagggcc gaggagcgcg gcggccagag 100
cgggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggccgtg 250
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cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
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gcctccaaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250

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 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20				25						30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35				40						45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50				55						60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65				70						75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
				350					355					360					
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln												

<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
cttcctctgt gggtaggacca tgtg 24

<210> 299
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gccacctcca tgctaacgcg g 21

<210> 300
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 300
ccaaggctcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301
<211> 1334
<212> DNA
<213> Homo sapiens

<400> 301
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tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150
tcagtttgtc ttgtgggggtt ggtggcaggc aggccggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
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gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
 tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
 ctggcctgac agaattcat cttgtttaat gctctcataa gaccacttgt 650
 ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
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 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggttaggg ccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gccaggttg ggcattctta acaaactccc acgtgatgct gatgctggtc 1000
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 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
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 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				65					70					75	
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr	
				80					85					90	
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln	
				95					100					105	
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu	
				110					115					120	
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr	
				125					130					135	
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu								
				140											

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200
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 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
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 ggcgatggct ccactgccc aggcacagc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600
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 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

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 ctccccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150
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 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
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<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35				40						45

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50				55						60

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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<400> 305
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ccgccttcgc cactggcctc ttctgggga ggcggtgcc cccatggcga 200
ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250
gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300
ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350
caggcccagc tcttgccaa cctggcgcg ctcatccagg ccaagaaggc 400
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cgctgcccgc ggacgggcgc gtggtgacct gcgaggtgga cgcgcagccc 500
ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550
cgacctccgg ctgaagcccg ccttgagac cctggacgag ctgctggcgg 600
cgggcgaggc cggcaccttc gacgtggccg tggtgatgc ggacaaggag 650
aactgctccg cctactacga gcgctgcctg cagctgctgc gaccgcgagg 700
catcctcgcc gtctcagag tcctgtggcg cgggaagggtg ctgcaacctc 750
cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcata 800
cggcgggacg tcagggtcta catcagcctc ctgccctgg gcgatggact 850
caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989
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Leu Thr Leu Ala Phe Lys Ile
260

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250
aatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
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<212> DNA

<213> Homo sapiens

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<212> PRT

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His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp					
				740					745					750					
Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His					
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<210> 311

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 312
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 312
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<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	35	40	45	
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	50	55	60	
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	65	70	75	
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	80	85	90	
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	95	100	105	
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	110	115	120	
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	125	130	135	
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	140	145	150	

Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
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Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
				170					175					180	
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	
				185					190					195	
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	
				200					205					210	
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
				215					220					225	
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
				230					235					240	
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	
				245					250					255	
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	
				260					265					270	
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	
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Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	
				290					295					300	
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	
				305					310					315	
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly	
				320					325					330	
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	
				335					340					345	
Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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			20						25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
			35						40					45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
			140						145					150

Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
			155						160					165

Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
			170						175					180

Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
			185						190					195

Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
			200						205					210

Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
			215						220					225

Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
			230						235					240

Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
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245					250					255				
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				260					265					270
Ile	Leu	Gly	Ser	Gly	Glu	Glu	Gly	Pro	Gln	Val	Gly	Pro	Ser	Ala
				275					280					285
Ala	Gln	Thr	Leu	Arg	Ser	Phe	Cys	Ala	Trp	Gln	Arg	Gly	Leu	Asn
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Thr	Pro	Glu	Asp	Ser	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu
				305					310					315
Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	Leu
				320					325					330
Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys
				335					340					345
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala
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His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys
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Pro	Cys	Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val
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Met	Ala	Pro	Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser
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Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr
				410					415					420
Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro
				425					430					435
Val	Thr	Phe	Pro	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln
				440					445					450
Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro
				455					460					465
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala
				470					475					480
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys
				485					490					495
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp
				500					505					510
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro
				515					520					525
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val

530										535					540				
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly					
				545					550					555					
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn					
				560					565					570					
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu					
				575					580					585					
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe					
				590					595					600					
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro					
				605					610					615					
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr					
				620					625					630					
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser					
				635					640					645					
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala					
				650					655					660					
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys					
				665					670					675					
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly					
				680					685					690					
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile					
				695					700					705					
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro					
				710					715					720					
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser					
				725					730					735					
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp					
				740					745					750					
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr					
				755					760					765					
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro					
				770					775					780					
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg					
				785					790					795					
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro					
				800					805					810					
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu					

815

820

825

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<210> 318

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

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<210> 319

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctgtgctctt cggcgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

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<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgttttgta tcctggccct aactctaatt gtcctgtttt 200

gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaat ggcactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
 gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
 attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
 ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
 aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80										85					90				
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe					
				95					100					105					
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys					
				110					115					120					
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro					
				125					130					135					
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe					
				140					145					150					
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn					
				155					160					165					
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn					
				170					175					180					
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu					
				185					190					195					
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala					
				200					205					210					
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro					
				215					220					225					
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu					
				230					235					240					
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe					
				245					250					255					
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg					
				260					265					270					
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly					
				275					280					285					
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys					
				290					295					300					
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly					
				305					310					315					

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
 accaacaatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
1					5				10					15

Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230	235	

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155					160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170					175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185					190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200					205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215					220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230					235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
				245					250					255
Ser	Lys	His	Asp	Tyr	Val									
				260										

<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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<211> 225

<212> PRT

<213> Homo sapiens

<400> 328

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Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp
				20					25					30
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn
				35					40					45
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile
				50					55					60
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met
				80					85					90
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr
				95					100					105
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu
				110					115					120
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile
				125					130					135
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn
				140					145					150
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu
				155					160					165
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala
				170					175					180
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr
				185					190					195
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His
				200					205					210
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50

ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100
gaccgctttc atcggaaca gcatcgtggt ggcccagggt gtgtgggagg 150
gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200
gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
ttgtggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
cgcttgtgc tcacctctgg gattgtcttt gtcactctag gggtcctgac 400
gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
accccttgtt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
ttgggctggg cggcctcagg cttttgttg ctgggtgggg gggtgctgtg 550
ctgcacttgc cctcggggg ggtcccagg cccagccat tacatggccc 600
gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
gagccatcca gaagtggcag tgcccaacag ctttgggatg gggtcgtacc 750
ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
tgcgagggt gcttgcgtg ctggctttgc aacaagacag actgtcccca 1000
agagttcctg ctgctgctgg gggctgggt tccctagatg tcaactggaca 1050
gctgcccccc atcctactca ggtctctgga gctcctctct tcaccttg 1100
aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
cctctgtttc ctccgtctg ataagacgtc cccccccag ggccagggtcc 1200
cagctatgta gacccccgc cccacctcca aactgcacc cttctgccct 1250
gccccctcg tctaccccc ttacactca catttttatc aaataaagca 1300
tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15
Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaaggaga acatcatcaa agactttctt agactcaaaa ggcttccacg 50

ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100

gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
 gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggg 200
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
 ggaagggctc tggatgaatt gcatccgaca agccaggggc cggttgcaat 300
 gcaagttcta tagctccttg ttggctctcc cgcctgccct ggaaacagcc 350
 cgggcctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
 tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagaggg 450
 ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
 atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
 tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
 cacttttcct tggctgggca agcgtgctg tcctcttcat tggagggggg 650
 ctgctttgtg gatthtgtg ctgcaacaga aagaagcaag ggtacagata 700
 tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
 caatgcttag taagacctcc accagttatg tctaattgct ccttttggct 800
 ccaagtatgg actatgggtca atgtttttta taaagtcctg ctagaaactg 850
 taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
 cgaaagtthc aatttggtac tgggtggtagg aatgaaaatg acttacttgg 950
 acattctgac ttcagtggtg ttaaattgcat tgactattgt tggacccaat 1000
 cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050
 caagtgtaca atgatggact acttattact ttttgacat catgtattat 1100
 ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
 acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1				5					10					15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala	Leu	Met	Cys	Val	Ala	Val	Ala	Leu	Ser	Leu	Ile	Ala	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450
ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500
ttttaaacac gtcaataaaa aaataatctc ccaga 535

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<210> 334
<211> 85
<212> PRT
<213> Homo sapiens

<400> 334
Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15
Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75
Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335
<211> 742
<212> DNA
<213> Homo sapiens

<400> 335
cccgcgcccc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50
ctgctcgcgc cccgccgcca tggctgcctc ccccgcgcg cctgctgtcc 100
tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200
tggtccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaata 550
agcgattctc ttcattgtat tcctaattgcc ttacactact tggtttctga 600
tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaattgcct tttgatattt catgggaatg 700

cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly
1				5					10					15
Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser
				20					25					30
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
				35					40					45
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
				50					55					60
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
				65					70					75
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
				80					85					90
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
				95					100					105
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
				110					115					120
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
				125					130					135
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr		
				140					145					

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

cggtctgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50

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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150

ttctggtgct ggcccttgcc tgggtctcaa cgacaccgc tgagggcggg 200

gaccactgc ccagccgtc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300


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ccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
gctacggctg aaattcctca atgattcaga gcagggtggc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
cagcagggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
gacctggggc agccttcacc tccctccaa ctgcgttctc cactgccacg 600
tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650
cccgccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
cctgctgttg ctgctgctct ggtactgcc aatccagtac cggcccttct 750
ttccctgac cgccactctg ggccctggccg gcttcaccct gctcctcagt 800
ctcctggcct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850
agcgtcgccg gccctcccg accttgctcc ccgcgcgcgc gcgggagctg 900
ctgcctgcc agggccgcct ctcgggctg cctcttccc ctgccctgga 950
gcccagccct gcgccgcaga ggactcccgc gactggcgga ggccccgccc 1000
tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
cgcactggga gtgggctcct cggggtcggg catctgctgt cgctgcctcg 1100
gccccgggca gagccgggccc gccccggggg cccgtcttag tgttctgccg 1150
gaggaccag ccgcctccaa tccctgacag ctccttgggc tgagttgggg 1200
acgccaggtc ggtgggaggc tggggaaggg gagcggggag gggcagagga 1250
gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
aaaaaaaaa 1310

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<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5					10					15
Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttggg tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
 gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550
 caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
 ccttccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
 tcttggttc ctccttactc ccatctggac ccagtccct ggttcctgtc 800
 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala	1	5	10	15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val	20	25	30	
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser	35	40	45	
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser	50	55	60	
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe	65	70	75	
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser	80	85	90	
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn	95	100	105	
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala	110	115	120	
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly	125	130	135	

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctatattata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val	560	565	570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln	575	580	585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser	590	595	600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu	605	610	615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe	620	625	630
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg							635		

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 350
 tatgtcgtg cgaggtggtg aaaacctga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351

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tccctctctg gccactgctg ttgctgcccc tcccacccgc tgctcagggc 150
tcttcacact cccctcgaac cccaccagcc ccagcccgc ccccggtgtgc 200
caggggaggg ccctcggccc caggtcatgt gtgcgtgtgg gagcgagcac 250
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

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Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
								20			25			30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggccgggtcg tggggcccg cgctatcgcg gccatcgtga 350
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser	1	5	10	15
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu	20	25	30	
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly	35	40	45	
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp	50	55	60	
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser	65	70	75	
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro	80	85	90	
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys	95	100	105	
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala	110	115	120	

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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 gttggccggc ggccgggccc gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcttgg 200
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggttat ttccccaacg agctgcgaaa 400
catcttcgag gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggagctgg ggaggagggc agctctccag ggagggaccc 500
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tggcatcttc cagtacgaga ccatctctg caacaactgc acagactcgc 750
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accgtgccca gggccctact gtccctgggg tcccaggctc tccttgagg 850
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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	1	5	10	15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	20	25	30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln				

	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
	140		145		150
Ser Pro Arg Gly Asp Leu Pro					
	155				

<210> 357
 <211> 1536
 <212> DNA
 <213> Homo sapiens

<400> 357
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 acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
 cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
 gcatggtgca aaaattccca ggcggtgcat ttgggatcag cactgattct 300
 gaggttctga cactacaa catcactggg aacaccatct gcctctttcg 350
 cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
 ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
 gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
 tcagattcat ctctcctga taatgaacaa ggctcccca gagtatgaag 550
 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
 ctctttattc tgggtggacag tggtagaaa gaaaatggga aggtgatatc 650
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 catgtgcaaa acttttgtga tggattccta agtggaatat tgttgaaaga 800
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 aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950
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 gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
 tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200
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cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450
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caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 359
 ccagcagtgccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 360
 tgacgagtggtacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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agtggctgga cgatggcagc gtccgcggga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcggggtga cctcagtcct ctggagcttc cagccagagg 400
gggcgacac tactgtgtcg tttttccact actccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
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 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp	1	5	10	15
Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu	20	25	30	
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu	35	40	45	
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe	50	55	60	
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser	65	70	75	
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr	80	85	90	

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	95	100	105
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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ccatcagcgc gccgggctgc cgctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
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gcctctggcc gagccgccac aggagcagtc cctcgcccc tggtctccgc 300
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agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

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agtgggttga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
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 cgaattgcta gcatcagcaa aagtctcacc atgggtgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
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 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
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 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
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<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15

Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagagaa gtctggctcag aaggttttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttggtt cattctcctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

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 1           5           10          15

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Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
          20          25          30

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Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu				35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe				50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu				65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu				80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn				95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp				110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys				125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val				140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro				155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu				170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly				185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala				200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys				215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser				230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly				245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu					260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

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ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
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cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttcggg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgcccctga gctgtaaccc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagttcc 1650
 ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700
 aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	1	5	10	15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	20	25	30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	35	40	45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	50	55	60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	65	70	75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	80	85	90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	95	100	105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	110	115	120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	125	130	135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	140	145	150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	155	160	165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	170	175	180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	185	190	195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	200	205	210	

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

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gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100
gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250
ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca ggcacagct gacatccccg cctcttctt gctcggccga 500
gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
tttgggcggt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
cccaggggcc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggct tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccagggtt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

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<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

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Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
 1             5             10             15

Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
                20             25             30

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
          35             40             45

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Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	
				50					55					60	
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	
				65					70					75	
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	
				80					85					90	
Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln	
				95					100					105	
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

<210> 377

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 396

<223> unknown base

<400> 377

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ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
ctggccctac ggctgtcact gggactagg tggcagaggc caaccctaaag 200
atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
aagaccagga ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
ttgtatgatg ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15

Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
			110						115	

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
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ggcgatgtgg agggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gcccacctg ggcaggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450
tttggaagc ttgatggcca gatctcctct gcctaccca gccaagaggg 500
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggatatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly	
				20					25					30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	
				35					40					45	
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	
				50					55					60	
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	
				65					70					75	
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	
				80					85					90	
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	
				95					100					105	
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	
				110					115					120	
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	
				125					130					135	
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	
				140					145					150	
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	
				155					160					165	
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			
				170					175						

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
cccccccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400
tgtcagcgag ccctgactca ctacagtgca gctgacaggg gctgtcatgc 450

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aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
cgaggatgcc ctaagggtg taggtgtgaa ggcaaaatgg tatattgtga 650
atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggtca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
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gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
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aacctggaac ttttgacct gggatataac cggatccgaa gtttagccag 1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
cagaaccttt acttgcatg gaataaaatc agtgatcatag gacagaccat 1250
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cgctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400
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aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
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ctcgtcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900

aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
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 ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150
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 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	

Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu	200	205	210
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	215	220	225
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	230	235	240
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	245	250	255
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	260	265	270
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	275	280	285
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	290	295	300
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	305	310	315
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	320	325	330
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	335	340	345
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	350	355	360
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu	365	370	375
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu	380	385	390
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly	395	400	405
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile	410	415	420
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu	425	430	435

Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys	440	445	450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys	455	460	465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr	470	475	480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu	485	490	495
Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu	500	505	510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389

agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaataatg tcaagatcca gaattttcag tgtcacctca 100
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200
aacaccctaa tggctggtat atctggatcc tcttctgct ggttttggtg 250
gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
gagaccccgga attgattctc acaggcgcac catggcagtt tttgctgttg 350
gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttcttctcc 450
atgttttggc cttttaggt cccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg aaaaagaat 650
ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
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gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
tctgctttaa actctttcct agcatgggt ccataaaaat tattataatt 900
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agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
tgaggttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
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tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
ctccatagtc catagtgttt ctctggagcc tcagggttg gcatttattg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390
<211> 146
<212> PRT
<213> Homo sapiens

<400> 390
Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
1 5 10 15
Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu
50 55 60
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 391
cttttcagtg tcacctcagc gatctc 26

<210> 392
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

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gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaaagtc agatgccct tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
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gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttggg ctcatattggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
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cagtaaccac aaataaaaaga acgaatgtct cgggcagtat cagatagcag 850
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<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
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Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25					30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40					45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55					60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70					75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85					90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100					105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115					120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130					135
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 396

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gggcccagac aaccgggcca tgcttccccg ggtgccaatg cgaggtggag 150

accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200

cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250

tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300

gggcccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350

caccagcatc tcaccactg ccttctcccg ccttcgctac ctggagtcgc 400

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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln	
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				20				25						30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35				40						45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50				55						60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65				70						75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80				85						90

Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser	95	100	105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	110	115	120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp	125	130	135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala	140	145	150
Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser	155	160	165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly	170	175	180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg	185	190	195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu	200	205	210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe	215	220	225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln	230	235	240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly	245	250	255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala	260	265	270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp	275	280	285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu	290	295	300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg	305	310	315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	320	325	330
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser	335	340	345
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu								350		

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

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cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

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ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

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 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25				30	

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40				45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	50	55	60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	65	70	75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	80	85	90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
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tcacaaaaac tcgactcaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
cacccgccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
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caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
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<210> 406
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 406

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Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg
305 310 315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

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tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200

agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcattg 350

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ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
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tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
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tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900
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agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
ttttttggta aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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  1               5               10               15

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Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
      20               25               30

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Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
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<210> 411
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 411
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<210> 412
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 413
atggcaggct tcctagataa ttttcggttg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgtg gaccacctcg ctttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
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tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
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aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
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gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
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gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag ccagacaca aacaaatacg agggatggcc agagctgctg 950
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tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

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Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
attctctcca cagacagctg gttc 24

<210> 421

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
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cacgccagga gctcgctcgc tctctctctc tctctctcac tctccctcc 200
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cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
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 tttccctaga tatactgcgg gatctctcct taggataaag agttgctggt 1650
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
 t 1701

<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

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Ala	Asp	Gly	Gly	Gln	His	Trp	Thr	Tyr	Glu	Gly	Pro	His	Gly	Gln
				20				25					30	
Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln
				35				40					45	
Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp
				50				55					60	
Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu
				65				70					75	
Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu
				80				85					90	

Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala	95	100	105
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly	110	115	120
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His	125	130	135
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala	140	145	150
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu	155	160	165
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His	170	175	180
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro	185	190	195
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe	200	205	210
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val	215	220	225
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln	230	235	240
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro	245	250	255
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn	260	265	270
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr	275	280	285
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly	290	295	300
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile	305	310	315
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser	320	325	330
Ala	Gln	Ala	Thr	Thr	Glu	Ala									335		

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 424
 gtaaagtcgc tggccagc 18

 <210> 425
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 425
 cccgatctgc ctgctgta 18

 <210> 426
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 426
 ctgcactgta tggccattat tgtg 24

 <210> 427
 <211> 45
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 427
 cagaacccta tgatacccta ctgaacaccg aatcccctgg aagcc 45

 <210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

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 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150
 aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300

ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350
 gggttgaatg tacaacagca actgcaccca catgtgttac caatttttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcaccttg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
 agcaaattgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
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<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
				20					25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
				35					40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
				50					55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
				65					70					75
Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu	Ser Ser Glu Glu Leu	Pro
	110	115	120
Gln Ile Phe Thr	Ser Leu Ile Ile His	Ser Leu Phe Pro Gly	Gly
	125	130	135
Ile Leu Pro Thr	Ser Gln Ala Gly Ala	Asn Pro Asp Val Gln	Asp
	140	145	150
Gly Ser Leu Pro	Ala Gly Gly Ala Gly	Val Asn Pro Ala Thr	Gln
	155	160	165
Gly Thr Pro Ala	Gly Arg Leu Pro Thr	Pro Ser Gly Thr Asp	Asp
	170	175	180
Asp Phe Ala Val	Thr Thr Pro Ala Gly	Ile Gln Arg Ser Thr	His
	185	190	195
Ala Ile Glu Glu	Ala Thr Thr Glu Ser	Ala Asn Gly Ile Gln	
	200	205	

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 <211> 1257
 <212> DNA
 <213> Homo Sapien

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 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgtc gagcgctctt gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttgggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650
 attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

aattaatatt catgcactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctottttt 900
ttattatgcc ttggaatggt tcaacttaaat gacattttta ataatgttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
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<210> 431

<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

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Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

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<213> Artificial Sequence

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<400> 432

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<400> 433

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<210> 434

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<212> DNA

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atgacgctcg tccaaggcca c 21

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cccacctgta ccaccatgt 19

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actccaggca ccattctgttc tccc 24

<210> 437
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tgacctggca aaggaagaa 19

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cagccaccct ccagtccaag g 21

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gggtcgtgtt ttggagaga 19

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<210> 443
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<400> 443
ctggcaggag ttaaagttcc aaga 24

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aaaggacacc gggatgtg 18

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<400> 446
caattctgga tgaggtggta ga 22

<210> 447
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<211> 23

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<210> 452

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<210> 454

<211> 21

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<210> 455

<211> 23

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<213> Artificial Sequence

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<210> 457
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<210> 458
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tagcagctgc ccttggtta 18

<210> 459
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aacagcaggt gcgactcatc ta 22

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tgctaggcga cgacacccag acc 23

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<210> 463
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<210> 467
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<210> 470
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<210> 471
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<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24

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<210> 473

<211> 19

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 473

aaggccaagg tgagtccat 19

<210> 474

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 474

cctactgagg agccctatgc 20

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<210> 476

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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gggaggctta taggccaat ctgg 24

<210> 477

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<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

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